

A. DEC100X

1644

P#6

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/382,088

DATE: 05/09/2000  
TIME: 06:36:01

Input Set: I382088.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

PS

1 <110> APPLICANT: Hope, Ernest G  
2 Negrin, Robert  
3 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTECTING ORGANS, TISSUE  
4 AND CELLS FROM IMMUNE SYSTEM-MEDIATED DAMAGE  
5 <130> FILE REFERENCE: A-67031-1/RFT  
6 <140> CURRENT APPLICATION NUMBER: US/09/382,088  
7 <141> CURRENT FILING DATE: 1999-08-24  
8 <150> EARLIER APPLICATION NUMBER: 60/097,640  
9 <151> EARLIER FILING DATE: 1998-08-24  
10 <160> NUMBER OF SEQ ID NOS: 30  
11 <170> SOFTWARE: PatentIn Ver. 2.1  
12 <210> SEQ ID NO 1  
13 <211> LENGTH: 9  
14 <212> TYPE: PRT  
15 <213> ORGANISM: Artificial Sequence  
16 <220> FEATURE:  
17 <221> NAME/KEY: SITE  
18 <222> LOCATION: (1)  
19 <223> OTHER INFORMATION: X at position 1 can be V, L, A or T.  
20 <220> FEATURE:  
21 <221> NAME/KEY: SITE  
22 <222> LOCATION: (2)  
23 <223> OTHER INFORMATION: X at position 2 can be L or H.  
24 <220> FEATURE:  
25 <221> NAME/KEY: SITE  
26 <222> LOCATION: (3)  
27 <223> OTHER INFORMATION: X at position 3 can be S or V.  
28 <220> FEATURE:  
29 <221> NAME/KEY: SITE  
30 <222> LOCATION: (4)  
31 <223> OTHER INFORMATION: X at position 4 can be D or E.  
32 <220> FEATURE:  
33 <221> NAME/KEY: SITE  
34 <222> LOCATION: (5)  
35 <223> OTHER INFORMATION: X at position 5 can be Q, K or R.  
36 <220> FEATURE:  
37 <221> NAME/KEY: SITE  
38 <222> LOCATION: (6)  
39 <223> OTHER INFORMATION: X at position 6 can be L or V.  
40 <220> FEATURE:  
41 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus  
42 sequence.  
43 <400> SEQUENCE: 1  
44 Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg

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45                   1                   5

46 <210> SEQ ID NO 2

47 <211> LENGTH: 9

48 <212> TYPE: PRT

49 <213> ORGANISM: Artificial Sequence

50 <220> FEATURE:

51 <221> NAME/KEY: SITE

52 <222> LOCATION: (1)..(3)

53 <223> OTHER INFORMATION: X at positions 1, 2, or 3 can be any amino acid.

54 <220> FEATURE:

55 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus

56 sequence.

57 <400> SEQUENCE: 2

58       Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg

59                   1                   5

60 <210> SEQ ID NO 3

61 <211> LENGTH: 9

62 <212> TYPE: PRT

63 <213> ORGANISM: Homo sapiens

64 <400> SEQUENCE: 3

65       Ala Val Leu Ser Ala Glu Gln Leu Arg

66                   1                   5

67 <210> SEQ ID NO 4

68 <211> LENGTH: 1254

69 <212> TYPE: DNA

70 <213> ORGANISM: Homo sapiens

71 <400> SEQUENCE: 4

72       cggtccact tctttggaca tctccggcgt cggggaccat gacgcctctt cgactcaagg 60

73       ttccgctggt gtgaccgtct cgggctcgtgt ccggaccgga agtcggacat agtccgttac 120

74       cggttcctgt gtccgtcacc tctttagtaga ccacagtggg caccaccacc ggagcagcga 180

75       cccagagcac agcgaccgcg cggtccgctg gtgccgcagc gtccggttcc gtcacgactc 240

76       gcggctcctc acgcgagaga ggaagaccgc tggaaatagg aggaccgaca ccgggaccgt 300

77       gacgcgctgc tctccacgt gcggccggac ccactcgacg acgcgagtga gtcgttgagc 360

78       tgccgcgctg tgcactggac ctccgaccgc tcggctgaca tgctgggtc gagtactcgc 420

79       aagcgactac tgaagcacgc gtcgtcgttc gtcgtgatgt tgacgctcgt gaggttctag 480

80       ttgaagggcc tgcgcgctcg cgcgacgtca ggtagtgtgt caccgcgcgc gtcgcccgcg ggacgatcag 600

81       ctgccgttcg acgggtcca gtggttcctg cacctcgcgt gctcgcgcgc ggacgatcag 660

82       ttgcggtaca agaagttcgg tgtgacccta ctctttaagg tgggtgttcta ccactgttg 720

83       gcaccgaagt accactgagc caggatatga caccacaat gctactacgt ggctgttcg 780

84       gagatgttga tgatgctgct gctcttcctc ttcgacgtcg accacctcta cggggaccga 840

85       gtgttcgaga ggtcggagta gtaggagtag ggggtagtgc acctcgagga gtcgcggaa 900

86       cttttcgacg attggtttct cgtcgacttc tagacctacc cttctacgt cttcttccga 960

87       caacggtaga ggaacgggtt cccacaccac ctccactggg tactggacgt ctttgtggac 1020

88       cgaccgcgacc cggactgact ccggttaactg ttcttgttcc ggctgaatag tgcgtacaga 1080

89       ccgttcttcc tagacatgga ccggtcacac aaggtgcggt ggcggaaact caacctgtgt 1140

90       ctaccgttgg ggaaactggt cctgtagatg cccgcgctcc tcgacgcgtc ggggttcgac 1200

91       aagatgcggc tgggtgggaa gtagaaggac cagccctgt ggggttcgcc gagggacgat 1254

92       aagtaaccgc cggaccaggc cgagttccca ctgttctacg ctctgctcaa tate

93 <210> SEQ ID NO 5

94 <211> LENGTH: 1254

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95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
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98 <221> NAME/KEY: CDS
99 <222> LOCATION: (1)..(1251)
100 <400> SEQUENCE: 5
101   atg cgc tct ctc ctt ctg ggc acc tta tgc ctc ctg gct gtg gcc ctg   48
102   Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
103       1               5               10               15
104   gca gcc gag gtg aag aaa cct gta gag gcc gca gcc cct ggt act gcg   96
105   Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
106       20               25               30
107   gag aag ctg agt tcc aag gcg acc aca ctg gca gag ccc agc aca ggc
108   Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
109       35               40               45
110   ctg gcc ttc agc ctg tat cag gca atg gcc aag gac cag gca gtg
111   Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
112       50               55               60
113   aac atc ctg gtg tca ccc gtg gtg gtg gcc tcg tcg ctg ggt ctc gtg
114   Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
115       65               70               75               80
116   tcg ctg ggc ggc aag gcg acc acg gcg tcg cag gcc aag gca gtg ctg   288
117   Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
118       85               90               95
119   agc gcc gag cag ctg cgc gac gag gag gtg cac gcc ggc ctg ggt gag   336
120   Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
121       100              105              110
122   ctg ctg cgc tca ctc agc aac tcg acg gcg cgc aac gtg acc tgg aag   384
123   Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
124       115              120              125
125   ctg ggc agc cga ctg tac gga ccc agc tca gtg agc ttc gct gat gac   432
126   Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
127       130              135              140
128   ttc gtg gcg agc agc aag cag cac tac aac tgc gag cac tcc aag atc   480
129   Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
130       145              150              155              160
131   aac ttc ccg gac aag cgc agc gcg ctg cag tcc atc aac gag tgg gcc   528
132   Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
133       165              170              175
134   gcg cag acc acc gac ggc aag ctg ccc gag gtc acc aag gac gtg gag   576
135   Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
136       180              185              190
137   agc acg gac ggc gcc ctg cta gtc aac gcc atg ttc ttc aag cca cac   624
138   Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
139       195              200              205
140   tgg gat gag aaa ttc cac cac aag atg gtg gac aac cgt ggc ttc atg   672
141   Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
142       210              215              220
143   gtg act cgg tcc tat act gtg ggt gtt acg atg atg cac cgg aca ggc   720
144   Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly

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145      225      230      235      240
146      ctc tac aac tac tac gac gac gag aag gag aag ctg cag ctg gtg gag 768
147      Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
148      245      250      255
149      atg ccc ctg gct cac aag ctc tcc agc ctc atc atc ctc atg ccc cat 816
150      Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
151      260      265      270
152      cac gtg gag cct ctc gag cgc ctt gaa aag ctg cta acc aaa gag cag 864
153      His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
154      275      280      285
155      ctg aag atc tgg atg ggg aag atg cag aag aag gct gtt gcc atc tcc 912
156      Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
157      290      295      300
158      ttg ccc aag ggt gtg gtg gag gtg acc cat gac ctg cag aaa cac ctg 960
159      Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
160      305      310      315      320
161      gct ggg ctg ggc ctg act gag gcc att gac aag aac aag gcc gac tta 1008
162      Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu
163      325      330      335
164      tca cgc atg tct ggc aag aag gat ctg tac ctg gcc agt gtg ttc cac 1056
165      Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His
166      340      345      350
167      gcc acc gcc ttt gag ttg gac aca gat ggc aac ccc ttt gac cag gac 1104
168      Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp
169      355      360      365
170      atc tac ggg cgc gag gag ctg cgc agc ccc aag ctg ttc tac gcc gac 1152
171      Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp
172      370      375      380
173      cac ccc ttc atc ttc ctg gtg cgg gac acc caa agc ggc tcc ctg cta 1200
174      His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu
175      385      390      395      400
176      ttc att ggg cgc ctg gtc cgg ctc aag ggt gac aag atg cga gac gag 1248
177      Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
178      405      410      415
179      tta tag
180      Leu 1254
181      <210> SEQ ID NO 6
182      <211> LENGTH: 417
183      <212> TYPE: PRT
184      <213> ORGANISM: Homo sapiens
185      <400> SEQUENCE: 6
186      Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
187      1 5 10 15
188      Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
189      20 25 30
190      Glu Lys Leu Ser Ser Lys Ala Thr Leu Ala Glu Pro Ser Thr Gly
191      35 40 45
192      Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
193      50 55 60
194      Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val

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195 65 70 75 80  
196 Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu  
197 85 90 95  
198 Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu  
199 100 105 110  
200 Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys  
201 115 120 125  
202 Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp  
203 130 135 140  
204 Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile  
205 145 150 155 160  
206 Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala  
207 165 170 175  
208 Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu  
209 180 185 190  
210 Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His  
211 195 200 205  
212 Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met  
213 210 215 220  
214 Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly  
215 225 230 235 240  
216 Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu  
217 245 250 255  
218 Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His  
219 260 265 270  
220 His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln  
221 275 280 285  
222 Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser  
223 290 295 300  
224 Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu  
225 305 310 315 320  
226 Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu  
227 325 330 335  
228 Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His  
229 340 345 350  
230 Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp  
231 355 360 365  
232 Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp  
233 370 375 380  
234 His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu  
235 385 390 395 400  
236 Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu  
237 405 410 415  
238 Leu  
239 <210> SEQ ID NO 7  
240 <211> LENGTH: 9  
241 <212> TYPE: PRT  
242 <213> ORGANISM: Artificial Sequence  
243 <220> FEATURE:  
244 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/382,088DATE: 05/09/2000  
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Line ? Error/Warning

Original Text

44 W "N" or "Xaa" used: Feature required  
58 W "N" or "Xaa" used: Feature required  
299 W "N" or "Xaa" used: Feature required  
321 W "N" or "Xaa" used: Feature required

Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg  
Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg  
Ala Val Leu Ser Ala Xaa Xaa Leu Arg  
Ala Xaa Leu Ser Ala Glu Xaa Xaa Arg